

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kossmann, Jens
Willmitzer, Lothar
Emmermann, Michael
- (ii) TITLE OF THE INVENTION: NUCLEIC ACID MOLECULES CODING FOR
DEBRANCHING ENZYMES FROM MAIZE
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: FISH & NEAVE
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10020-1104
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP97/01141
(B) FILING DATE: 06-MAR-97
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE 196 08 918.2
(B) FILING DATE: 07-MAR-96
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: Haley Jr., James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: GFB-7
- (x) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 596-9000
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1993 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(F) TISSUE TYPE: Blattgewebe

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGC	ACG	AGG	TCA	AAA	CTC	CCT	CCA	GGG	TCA	GAT	TTG	CAA	CAA	GCT	GCA	48
Gly	Thr	Arg	Ser	Lys	Leu	Pro	Pro	Gly	Ser	Asp	Leu	Gln	Gln	Ala	Ala	
1				5				10						15		
ATT	GTG	GCT	ATT	CAG	GAA	GAG	GAC	CCT	TAT	AAT	TGG	GGG	TAT	AAC	CCT	96
Ile	Val	Ala	Ile	Gln	Glu	Glu	Asp	Pro	Tyr	Asn	Trp	Gly	Tyr	Asn	Pro	
			20					25					30			
GTG	GTT	TGG	GGC	GTT	CCA	AAA	GGA	AGC	TAT	GCA	AGT	AAC	CCA	GAT	GGT	144
Val	Val	Trp	Gly	Val	Pro	Lys	Gly	Ser	Tyr	Ala	Ser	Asn	Pro	Asp	Gly	
			35					40					45			
CCA	AGT	CGT	ATC	ATT	GAG	TAC	CGG	CTG	ATG	GTG	CAG	GCC	TTG	AAT	CGC	192
Pro	Ser	Arg	Ile	Ile	Glu	Tyr	Arg	Leu	Met	Val	Gln	Ala	Leu	Asn	Arg	
			50				55					60				
TTA	GGT	CTT	CGA	GTT	GTC	ATG	GAT	GTT	GTA	TAC	AAT	CAT	CTA	TAC	TCA	240
Leu	Gly	Leu	Arg	Val	Val	Met	Asp	Val	Val	Tyr	Asn	His	Leu	Tyr	Ser	
	65				70					75					80	
AGT	GGC	CCT	TTT	GCC	ATC	ACT	TCC	GTG	CTT	GAC	AAG	ATT	GTA	CCT	GGA	288
Ser	Gly	Pro	Phe	Ala	Ile	Thr	Ser	Val	Leu	Asp	Lys	Ile	Val	Pro	Gly	
				85					90					95		
TAC	TAC	CTC	AGA	AGG	GAC	TCT	AAT	GGT	CAG	ACT	GAG	AAC	AGC	GCG	GCT	336
Tyr	Tyr	Leu	Arg	Arg	Asp	Ser	Asn	Gly	Gln	Thr	Glu	Asn	Ser	Ala	Ala	
			100					105					110			
GTG	AAC	AAT	ACA	GCA	AGT	GAG	CAT	TTC	ATG	GTT	GAT	AGA	TTA	ATC	GTG	384
Val	Asn	Asn	Thr	Ala	Ser	Glu	His	Phe	Met	Val	Asp	Arg	Leu	Ile	Val	
		115					120					125				
GAT	GAC	CTT	CTG	AAT	TGG	GCA	GTA	AAT	TAC	AAA	GTT	GAC	GGG	TTC	AGA	432
Asp	Asp	Leu	Leu	Asn	Trp	Ala	Val	Asn	Tyr	Lys	Val	Asp	Gly	Phe	Arg	
		130				135					140					
TTT	GAT	CTA	ATG	GGA	CAT	ATC	ATG	AAA	AAG	ACA	ATG	ATT	AGA	GCA	AAA	480
Phe	Asp	Leu	Met	Gly	His	Ile	Met	Lys	Lys	Thr	Met	Ile	Arg	Ala	Lys	
	145				150					155					160	
TCG	GCT	CTT	CAA	AGC	CTT	ACA	ATT	GAT	GAA	CAT	GGA	GTA	GAT	GGT	TCA	528
Ser	Ala	Leu	Gln	Ser	Leu	Thr	Ile	Asp	Glu	His	Gly	Val	Asp	Gly	Ser	
			165					170					175			
AAG	ATA	TAC	TTG	TAT	GGT	GAA	GGA	TGG	AAC	TTC	GGT	GAA	GTT	GCG	GAA	576
Lys	Ile	Tyr	Leu	Tyr	Gly	Glu	Gly	Trp	Asn	Phe	Gly	Glu	Val	Ala	Glu	
			180					185					190			
AAT	CAA	CGT	GGG	ATA	AAT	GGA	TCC	CAG	CTA	AAT	ATG	AGT	GGC	ACT	GGG	624
Asn	Gln	Arg	Gly	Ile	Asn	Gly	Ser	Gln	Leu	Asn	Met	Ser	Gly	Thr	Gly	
		195					200						205			

TTG GTT CCA GGA GTT ATT GTC ATG AGC ATC GAA GAT GCA CGA AAT GAT	1440
Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp	
465 470 475 480	
AGG CAT GAT ATG GCC CAG ATA GAT GAA ACA TTC TCT TGT GTC GTT ACA	1488
Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr	
485 490 495	
GTC TTC AAT GTA TGT CCG TAC GAA GTG TCT ATA GAA ATC CCT GAT CTT	1536
Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu	
500 505 510	
GCA TCA CTG CGG CTT CAG TTG CAT CCA GTG CAG GTG AAT TCA TCG GAT	1584
Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp	
515 520 525	
GCG TTA GCC AGG CAG TCT GCG TAC GAC ACC GCC ACA GGT CGA TTC ACC	1632
Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr	
530 535 540	
GTG CCG AAA AGG ACA GCA GCA GTG TTC GTG GAA CCC AGG TGC T	1675
Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys	
545 550 555	
GATGGATGCC TTTCGCTAGC GAGCAAGTGC ATTCGGCATC CAAGTCGAAG CAAACGAATG	1735
AAATAAGAGA AGGCCATCGA ATAAAACGAA GTATATAAAT AGATTGAATA AGACGTTGCC	1795
CAAGTTGCCA AGGCACGCTT TGCCATATGT ATGCGTTGAA AAATAAATAA ATAAATAAAT	1855
AAATGATGTT ATAGAGGTAC AAAAGCATTG GAACATTTCT TTATAGAGGT GAACCACCCT	1915
ATTTTCCAGT TTCCATGTGT GAATTGTGAT TAGCATATGT ATGGAATAAT AATATAAATT	1975
AATTTTATGC AAAAAAAA	1993

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala	
1 5 10 15	
Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro	
20 25 30	
Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly	
35 40 45	
Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg	
50 55 60	
Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser	
65 70 75 80	

Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly
 85 90 95
 Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala
 100 105 110
 Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val
 115 120 125
 Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg
 130 135 140
 Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys
 145 150 155 160
 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser
 165 170 175
 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu
 180 185 190
 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly
 195 200 205
 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser
 210 215 220
 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu
 225 230 235 240
 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr
 245 250 255
 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu
 260 265 270
 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser
 275 280 285
 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro
 290 295 300
 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe
 305 310 315 320
 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg
 325 330 335
 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly
 340 345 350
 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu
 355 360 365
 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe
 370 375 380
 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys
 385 390 395 400
 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser
 405 410 415

Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile
 420 425 430
 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr
 435 440 445
 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser
 450 455 460
 Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp
 465 470 475 480
 Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr
 485 490 495
 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu
 500 505 510
 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp
 515 520 525
 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr
 530 535 540
 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys
 545 550 555

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE DESCRIPTION:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Solanum tuberosum
 - (B) STRAIN: Berolina
 - (F) TISSUE TYPE: tuber
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LAGE:1..492
 - (D) OTHER INFORMATION:/product= "debranching enzyme (R-enzyme) "

(xi) SEQUENCE INFORMATION: SEQ ID NO: 3:

TCT GCT GAT GGC AAG TGG ACA TTA TTA GTT AAT CTT GAT TCT GAT GAT	48
Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp	
560 565 570	
GTA AAA CCT GAA GGC TGG GAT AAT CTA CAA GAC GTG AAG CCA AAT CTT	96
Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu	
575 580 585 590	

CTT	TCC	TTT	TCT	GAT	GTC	AGC	ATC	TAT	GAG	CTG	CAT	GTT	AGA	GAT	TTC	144
Leu	Ser	Phe	Ser	Asp	Val	Ser	Ile	Tyr	Glu	Leu	His	Val	Arg	Asp	Phe	
				595					600					605		
ACT	GCC	AGT	GAC	CCT	ACT	GTG	TCT	CAT	GAA	TTT	CAG	GCC	GGT	TAT	CTC	192
Thr	Ala	Ser	Asp	Pro	Thr	Val	Ser	His	Glu	Phe	Gln	Ala	Gly	Tyr	Leu	
			610					615					620			
GCC	CCT	TCC	ACG	TCG	CAG	GCA	TCA	GCT	GGT	GTC	CAA	CAT	TTG	AAA	AGA	240
Ala	Pro	Ser	Thr	Ser	Gln	Ala	Ser	Ala	Gly	Val	Gln	His	Leu	Lys	Arg	
		625					630					635				
TTA	TCA	AGT	GCT	GGT	ATC	ACT	CAT	GTC	CAC	CTG	TGG	CCA	ACC	TAT	CAA	288
Leu	Ser	Ser	Ala	Gly	Ile	Thr	His	Val	His	Leu	Trp	Pro	Thr	Tyr	Gln	
	640					645					650					
TTT	GCT	GGT	GTC	GAA	GAT	GAG	AAA	CAT	AAA	TGG	AAG	TAT	ACA	GAT	ATC	336
Phe	Ala	Gly	Val	Glu	Asp	Glu	Lys	His	Lys	Trp	Lys	Tyr	Thr	Asp	Ile	
655					660					665					670	
GAG	AAA	CTC	AAC	TCT	TTT	CCA	CCA	GAT	TCT	GAG	GAG	CAG	CAG	GCT	CTT	384
Glu	Lys	Leu	Asn	Ser	Phe	Pro	Pro	Asp	Ser	Glu	Glu	Gln	Gln	Ala	Leu	
			675						680					685		
ATC	ACA	GCC	ATC	CAA	GAT	GAA	GAT	GGC	TAT	AAT	TGG	GGG	TAT	AAT	CCT	432
Ile	Thr	Ala	Ile	Gln	Asp	Glu	Asp	Gly	Tyr	Asn	Trp	Gly	Tyr	Asn	Pro	
			690					695					700			
GTT	CTC	TGG	GGA	GTT	CCA	AAG	GGA	AGC	TAT	GCT	GGT	AAT	GCA	AAT	GGT	480
Val	Leu	Trp	Gly	Val	Pro	Lys	Gly	Ser	Tyr	Ala	Gly	Asn	Ala	Asn	Gly	
		705					710					715				
CCT	TGT	CGT	ATC													492
Pro	Cys	Arg	Ile													
	720															

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ser	Ala	Asp	Gly	Lys	Trp	Thr	Leu	Leu	Val	Asn	Leu	Asp	Ser	Asp	Asp	
1				5					10					15		
Val	Lys	Pro	Glu	Gly	Trp	Asp	Asn	Leu	Gln	Asp	Val	Lys	Pro	Asn	Leu	
		20						25					30			
Leu	Ser	Phe	Ser	Asp	Val	Ser	Ile	Tyr	Glu	Leu	His	Val	Arg	Asp	Phe	
		35					40					45				
Thr	Ala	Ser	Asp	Pro	Thr	Val	Ser	His	Glu	Phe	Gln	Ala	Gly	Tyr	Leu	
	50					55					60					
Ala	Pro	Ser	Thr	Ser	Gln	Ala	Ser	Ala	Gly	Val	Gln	His	Leu	Lys	Arg	
65					70					75					80	

Leu Ser Ser Ala Gly Ile Thr His Val His Leu Trp Pro Thr Tyr Gln
 85 90 95
 Phe Ala Gly Val Glu Asp Glu Lys His Lys Trp Lys Tyr Thr Asp Ile
 100 105 110
 Glu Lys Leu Asn Ser Phe Pro Pro Asp Ser Glu Glu Gln Gln Ala Leu
 115 120 125
 Ile Thr Ala Ile Gln Asp Glu Asp Gly Tyr Asn Trp Gly Tyr Asn Pro
 130 135 140
 Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala Gly Asn Ala Asn Gly
 145 150 155 160
 Pro Cys Arg Ile

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